

0260
DATE: 04/16/98
TIME: 13:47:14

INPUT SET: S25005.raw

This Raw Listing contains the General Information Section and up to the first 5 pages

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Weeks, Donald P.
Wang, Xiao-Zhuo
Herman, Patricia L.

9 (ii) TITLE OF INVENTION: "METHODS AND MATERIALS FOR MAKING AND
10 USING TRANSGENIC DICAMBA-DEGRADING ORGANISMS"

12 (iii) NUMBER OF SEQUENCES: 6

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Sheridan Ross P.C.
16 (B) STREET: 1700 Lincoln St., Suite 3500
17 (C) CITY: Denver
18 (D) STATE: Colorado
19 (E) COUNTRY: USA
20 (F) ZIP: 80203

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

29 (A) APPLICATION NUMBER:
30 (B) FILING DATE:
31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: US 60/042,666
35 (B) FILING DATE: 04-APR-1997

37 (vii) PRIOR APPLICATION DATA:

38 (A) APPLICATION NUMBER: US 60/042,941
39 (B) FILING DATE: 04-APR-1997

41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: Crook, Wannell M.
43 (B) REGISTRATION NUMBER: 31,071
44 (C) REFERENCE/DOCKET NUMBER: 3553-18

46 (ix) TELECOMMUNICATION INFORMATION:

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INPUT SET: S25005.raw

47 (A) TELEPHONE: (303) 863-9700
48 (B) TELEFAX: (303) 863-0223
49
50
51 (2) INFORMATION FOR SEQ ID NO:1:
52
53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 29 amino acids
55 (B) TYPE: amino acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear
58
59 (ii) MOLECULE TYPE: protein
60
61
62 (ix) FEATURE:
63 (A) NAME/KEY: Region
64 (B) LOCATION: 28
65 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Asp or
66 Thr"
67
68 (ix) FEATURE:
69 (A) NAME/KEY: Region
70 (B) LOCATION: 29
71 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Pro"
72
73
74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
75
76 Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu Leu
77 1 5 10 15
78
79 Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Xaa Xaa
80 20 25
81
82 (2) INFORMATION FOR SEQ ID NO:2:
83
84 (i) SEQUENCE CHARACTERISTICS:
85 (A) LENGTH: 20 amino acids
86 (B) TYPE: amino acid
87 (C) STRANDEDNESS: single
88 (D) TOPOLOGY: linear
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90 (ii) MOLECULE TYPE: protein
91
92
93 (ix) FEATURE:
94 (A) NAME/KEY: Region
95 (B) LOCATION: 8
96 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"
97
98 (ix) FEATURE:
99 (A) NAME/KEY: Region

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100 (B) LOCATION: 11
101 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"
102

103 (ix) FEATURE:
104 (A) NAME/KEY: Region
105 (B) LOCATION: 16
106 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"
107

108 (ix) FEATURE:
109 (A) NAME/KEY: Region
110 (B) LOCATION: 20
111 (D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"
112

113 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

114 Thr Tyr Val Val Thr Asp Ala Xaa Ile Lys Xaa Lys Tyr Met Asp Xaa
115 1 5 10 15

116 Val Glu Val Xaa
117 20

118 (2) INFORMATION FOR SEQ ID NO:3:

119 (i) SEQUENCE CHARACTERISTICS:
120 (A) LENGTH: 1020 base pairs
121 (B) TYPE: nucleic acid
122 (C) STRANDEDNESS: single
123 (D) TOPOLOGY: linear

124 (ii) MOLECULE TYPE: cDNA

125 (ix) FEATURE:
126 (A) NAME/KEY: CDS
127 (B) LOCATION: 1..1020

128 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

129 ATG ACC TTC GTC CGC AAT GCC TGG TAT GTG GCG GCG CTG CCC GAG GAA 48
130 Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu
131 1 5 10 15

132 CTG TCC GAA AAG CCG CTC GGC CGG ACG ATT CTC GAC ACA CCG CTC GCG 96
133 Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala
134 20 25 30

135 CTC TAC CGC CAG CCC GAC GGT GTG GTC GCG GCG CTG CTC GAC ATC TGT 144
136 Leu Tyr Arg Gln Pro Asp Gly Val Val Ala Ala Leu Asp Ile Cys
137 35 40 45

138 CCG CAC CGC TTC GCG CCG CTG AGC GAC GGC ATC CTC GTC AAC GGC CAT 192

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153	Pro His Arg Phe Ala Pro Leu Ser Asp Gly Ile Leu Val Asn Gly His			
154	50	55	60	
155				
156	CTC CAA TGC CCC TAT CAC GGG CTG GAA TTC GAT GGC GGC GGG CAG TGC	240		
157	Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gly Gln Cys			
158	65	70	75	80
159				
160	GTC CAT AAC CCG CAC GGC AAT GGC GCC CGC CCG GCT TCG CTC AAC GTC	288		
161	Val His Asn Pro His Gly Asn Gly Ala Arg Pro Ala Ser Leu Asn Val			
162	85	90	95	
163				
164	CGC TCC TTC CCG GTG GTG GAG CGC GAC GCG CTG ATC TGG ATC TGG CCC	336		
165	Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro			
166	100	105	110	
167				
168	GGC GAT CCG GCG CTG GCC GAT CCT GGG GCG ATC CCC GAC TTC GGC TGC	384		
169	Gly Asp Pro Ala Leu Ala Asp Pro Gly Ala Ile Pro Asp Phe Gly Cys			
170	115	120	125	
171				
172	CGC GTC GAT CCC GCC TAT CGG ACC GTC GGC GGC TAT GGG CAT GTC GAC	432		
173	Arg Val Asp Pro Ala Tyr Arg Thr Val Gly Gly Tyr Gly His Val Asp			
174	130	135	140	
175				
176	TGC AAC TAC AAG CTG CTG GTC GAC AAC CTG ATG GAC CTC GGC CAC GCC	480		
177	Cys Asn Tyr Lys Leu Leu Val Asp Asn Leu Met Asp Leu Gly His Ala			
178	145	150	155	160
179				
180	CAA TAT GTC CAT CGC GCC AAC GCC CAG ACC GAC GCC TTC GAC CGG CTG	528		
181	Gln Tyr Val His Arg Ala Asn Ala Gln Thr Asp Ala Phe Asp Arg Leu			
182	165	170	175	
183				
184	GAG CGC GAG GTG ATC GTC GGC GAC GGT GAG ATA CAG GCG CTG ATG AAG	576		
185	Glu Arg Glu Val Ile Val Gly Asp Gly Glu Ile Gln Ala Leu Met Lys			
186	180	185	190	
187				
188	ATT CCC GGC GGC ACG CCG AGC GTG CTG ATG GCC AAG TTC CTG CGC GGC	624		
189	Ile Pro Gly Gly Thr Pro Ser Val Leu Met Ala Lys Phe Leu Arg Gly			
190	195	200	205	
191				
192	GCC AAT ACC CCC GTC GAC GCT TGG AAC GAC ATC CGC TGG AAC AAG GTG	672		
193	Ala Asn Thr Pro Val Asp Ala Trp Asn Asp Ile Arg Trp Asn Lys Val			
194	210	215	220	
195				
196	AGC GCG ATG CTC AAC TTC ATC GCG GTG GCG CCG GAA GGC ACC CCG AAG	720		
197	Ser Ala Met Leu Asn Phe Ile Ala Val Ala Pro Glu Gly Thr Pro Lys			
198	225	230	235	240
199				
200	GAG CAG AGC ATC CAC TCG CGC GGT ACC CAT ATC CTG ACC CCC GAG ACG	768		
201	Glu Gln Ser Ile His Ser Arg Gly Thr His Ile Leu Thr Pro Glu Thr			
202	245	250	255	
203				
204	GAG GCG AGC TGC CAT TAT TTC TTC GGC TCC TCG CGC AAT TTC GGC ATC	816		
205	Glu Ala Ser Cys His Tyr Phe Phe Gly Ser Ser Arg Asn Phe Gly Ile			

RAW SEQUENCE LISTING
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206 260 265 270
207
208 GAC GAT CCG GAG ATG GAC GGC GTG CTG CGC AGC TGG CAG GCT CAG GCG 864
209 Asp Asp Pro Glu Met Asp Gly Val Leu Arg Ser Trp Gln Ala Gln Ala
210 275 280 285
211
212 CTG GTC AAG GAG GAC AAG GTC GTC GTC GAG GCG ATC GAG CGC CGC CGC 912
213 Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg
214 290 295 300
215
216 GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TCG TGC GAC 960
217 Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
218 305 310 315 320
219
220 GAA GCC GCA GTC CGT GTC AGC CGC GAG ATC GAG AAG CTT GAG CAG CTC 1008
221 Glu Ala Ala Val Arg Val Ser Arg Glu Ile Glu Lys Leu Glu Gln Leu
222 325 330 335
223
224 GAA GCC GCC TGA 1020
225 Glu Ala Ala *
226 340
227
228
229 (2) INFORMATION FOR SEQ ID NO:4:
230
231 (i) SEQUENCE CHARACTERISTICS:
232 (A) LENGTH: 339 amino acids
233 (B) TYPE: amino acid
234 (D) TOPOLOGY: linear
235
236 (ii) MOLECULE TYPE: protein
237
238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
239
240 Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu
241 1 5 10 15
242
243 Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala
244 20 25 30
245
246 Leu Tyr Arg Gln Pro Asp Gly Val Val Ala Ala Leu Leu Asp Ile Cys
247 35 40 45
248
249 Pro His Arg Phe Ala Pro Leu Ser Asp Gly Ile Leu Val Asn Gly His
250 50 55 60
251
252 Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gln Cys
253 65 70 75 80
254
255 Val His Asn Pro His Gly Asn Gly Ala Arg Pro Ala Ser Leu Asn Val
256 85 90 95
257
258 Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro

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SEQUENCE VERIFICATION REPORT
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Line	Error	Original Text
303	Stop Codon at end of sequence removed - no error	
389	Stop Codon at end of sequence removed - no error	